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09/665,308

BB11409 USNA

AMENDMENT

STATEMENT UNDER 37 CFR 1.821(g) AND 1.825(b)

SEQUENCE LISTING - CRF

SEQUENCE LISTING - 28 PAGES

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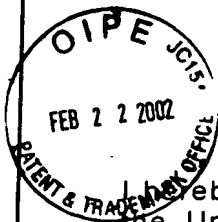
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09/665,308

BB1149 USNA

AMENDMENT

STATEMENT UNDER 37 CFR 1.821(g) AND 1.825(b)

SEQUENCE LISTING - CRF

SEQUENCE LISTING - 28 PAGES

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Burden Hour Statement: This form is estimated to take 0.03 hours to complete. Time will vary depending upon the needs of the individual case. Any comments on the amount of time you are required to complete this form should be sent to the Chief Information Officer, U.S. Patent and Trademark Office, Washington, DC 20231. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. SEND TO: Assistant Commissioner for Patents, Washington, DC 20231.



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Patent and Trademark Office  
COMMISSIONER OF PATENTS AND TRADEMARKS  
Washington, D.C. 20231

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/665308	09/19/2000	CAHOON, REBECCA E.	BB1149 US NA

EXAMINER	
Cynthia Collins	
ART UNIT	PAPER NUMBER
1638	13

Please find below a communication from the EXAMINER in charge of this application

The communication filed July 23, 2001 is not fully responsive to the Office communication mailed June 18, 2001 for the reason(s) set forth on the attached Notice To Comply With The Sequence Rules or CRF Diskette Problem Report. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

Since the above-mentioned reply appears to be *bona fide* attempt to comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825), applicant is given a TIME PERIOD of **ONE (1) MONTH** from the mailing date of this communication within which to correct the deficiency so as to comply with the sequence rules (37 CFR 1.821 - 1.825) in order to avoid abandonment of the application under 37 CFR 1.821(g). EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a).

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Examiner Cynthia Collins whose telephone number is (703) 605-1210. If the examiner cannot be reached, inquiries can be directed to Supervisory Patent Examiner Paula Hutzell whose telephone number is (703) 308-4310. The fax number for the organization where this application or proceeding is assigned is (703) 308-4242.

Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

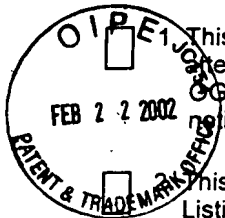
Cynthia Collins October 12, 2001

ELIZABETH F. McELWAIN  
PRIMARY EXAMINER  
GROUP 1600

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):



This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).

This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: \_\_\_\_\_

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**Applicant Must Provide:**

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- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

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# Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: <u>C9/665,308A</u>
<b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE</b>		
1 <u>    </u> Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <u>    </u> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <u>    </u> Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <u>    </u> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <u>    </u> Variable Length	Sequence(s) <u>        </u> contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <u>    </u> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) <u>        </u> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <u>    </u> Skipped Sequences (OLD RULES)	Sequence(s) <u>        </u> missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <u>    </u> Skipped Sequences (NEW RULES)	Sequence(s) <u>        </u> missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <u>    </u> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <u>    </u> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <u>    </u> Use of <220>	Sequence(s) <u>        </u> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <u>    </u> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <u>    </u> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

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8/16/01  
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RAW SEQUENCE LISTING

DATE: 07/31/2001

PATENT APPLICATION: US/09/665,308A

TIME: 14:45:58

Input Set : A:\BB1149USNA Corrected Seq List.txt

Output Set: N:\CRF3\07312001\I665308A.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: Cahoon, Rebecca E.  
 4 Klein, Theodore M.  
 5 Odell, Joan T.  
 6 Orozco, Emil M. Jr.  
 8 <120> TITLE OF INVENTION: PLANT CELL CYCLIN GENES  
 0 <130> FILE REFERENCE: BB1149 US NA  
 2 <140> CURRENT APPLICATION NUMBER: US/09/665,308A  
 2 <141> CURRENT FILING DATE: 2000-09-19  
 2 <150> PRIOR APPLICATION NUMBER: 60/078,735  
 3 <151> PRIOR FILING DATE: 1998 March 20 1998-03-20  
 5 <150> PRIOR APPLICATION NUMBER: PCT/US99/06047  
 6 <151> PRIOR FILING DATE: 1999 March 19 1999-03-19  
 8 <160> NUMBER OF SEQ ID NOS: 32  
 0 <170> SOFTWARE: MICROSOFT OFFICE 97

use this date format

## D SEQUENCES

053 <210> SEQ ID NO: 21  
 054 <211> LENGTH: 789  
 055 <212> TYPE: DNA  
 056 <213> ORGANISM: Triticum aestivum  
 058 <400> SEQUENCE: 21  
 059 cacctgaggg cgactcgagg gtgccctcgc cccgtccgcc gtgaccaccc ctcttcggat 60  
 060 ctcaccgcct cgacccaaat gtgatttgag gcaaattctg cgtttgaggc aaggacaata 120  
 061 aaagtgatgg agcttttggc cttcagcacc ttgaaatgga ggatgcaagc tgttactgct 180  
 062 tgctcggtta ttgactactt cctttgcaaa ttcaatgatc atgacacacc ctccatgctt 240  
 063 gcattctcct gctcaactga cctcatcctg agcacaaacta agtgagctga ttttttggtg 300  
 064 ttcagacatt cagagattgc tggaaagtgtt gcacttcctt catttgggga gcacaagact 360  
 065 tcagttgtcg aaatggctac aactaattgc aagtatataa acaaggaggc gtgatgtgac 420  
 066 aggaaagatc ctgatgaagt gcttccttta tggaaatgcct atctgaagtt tggactaaga 480  
 067 gacatgcttt aattggctta gtaaaaaata cttgctaaag agaaataaga ttcaaagtag 540  
 068 atgtttttat tgtagattag gatattgtgt ttctgccacc ggctcgactt ctcatattag 600  
 069 aaggcaagca gttagtccat atcttactat ttgcaactat tgtagatgga tggtagaggga 660  
 070 ttgagaggct actactatta atgtgcgtaa actttgcac tttagctctc taaatgaaac 720  
 071 cgggtgatgt taacctgaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 780  
 072 aaaaaaaaaa 789

789 ← insert

25 <210> SEQ ID NO: 23  
 26 <211> LENGTH: 603 1132 (p. 2)  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Zea mays  
 30 <220> FEATURE:  
 31 <221> NAME/KEY: unsure  
 32 <222> LOCATION: (441)  
 34 <220> FEATURE:  
 35 <221> NAME/KEY: unsure  
 36 <222> LOCATION: (447)

## RAW SEQUENCE LISTING

DATE: 07/31/2001

PATENT APPLICATION: US/09/635,308A

TIME: 14:45:58

Input Set : A:\BB1149USNA Corrected Seq List.txt

Output Set: N:\CRF3\07312001\I665308A.raw

```

1138 <220> FEATURE:
1139 <221> NAME/KEY: unsure
1140 <222> LOCATION: (485)
1142 <220> FEATURE:
1143 <221> NAME/KEY: unsure
1144 <222> LOCATION: (498)
1146 <220> FEATURE:
1147 <221> NAME/KEY: unsure
1148 <222> LOCATION: (528)
1150 <220> FEATURE:
1151 <221> NAME/KEY: unsure
1152 <222> LOCATION: (553)
1154 <220> FEATURE:
1155 <221> NAME/KEY: unsure
1156 <222> LOCATION: (560)
1158 <220> FEATURE:
1159 <221> NAME/KEY: unsure
1160 <222> LOCATION: (576)..(577)
1162 <220> FEATURE:
1163 <221> NAME/KEY: unsure
1164 <222> LOCATION: (598)
1166 <400> SEQUENCE: 23
1167 aacagaattc ggcacgagcc gcggtcggct gggtttcacg cgccgcggcg cggctaggct 60
1168 tctccgcgct caccgcgcgc ctcgcccgcg cctacctcga ccgctgcttc ctccccgggg 120
1169 gcgcgctccg gctcggcgac cagccctgga tggcgcgccct agccgcgcgc acctgcttcg 180
1170 cgctcgccgc caaggtcgag gagacgcgcg tgccgcgcgc cctcgacctc cagctctacg 240
1171 ccgcccgtga cgcgcgggat ccgtacgtat tcgaggccaa gacggtgcgc cggatggagc 300
1172 tgctcgtgct ctccgcgctt gggtagcgga tgcacctgt caccgcttc tctacctcc 360
1173 agcccgtcct cgccgacgct gcgacgcgcc tgcgtagctg cgagggcgct ctgctcgcg 420
1174 tcatggccga ctggaggtgg cctcggcacc ggccttcggc gtgggcccgc gccgcgttgc 480
1175 tgatcacagc cgccgcggcg gacggcgcg acggcgacgg cgacacggag ctctggcg 540
1176 tcatcaatgc ccccgaggac aagaccgcgc agtggtccaa gatcatctcc gaggtgacgg 600
1177 gcatgagctt cctcgctgc gatgtcggcg tgagcgccgc aaataagcgt aagcacgcgc 660
1178 cggcgagtt gtactcgccg ccgcccagcc cgagcgccgt gatcgccgc ctgtcctgct 720
1179 tcagctgcga gagctcgacg tccgccaccg ctatggctgc ggcggtcgc ccgtgggcgc 780
1180 cgtcggcgtc cgtgtccgtg tcgtcctctc cagagccacc aggtcgggcc cccaagcgcg 840
1181 cagcgccggc gtcggcgctg gcgtcggcgt cagccggggg cgccgccacc gtccaggtcc 900
1182 cgcacagct acccccgac gaggagagcc gcgacgcctg gccgtccacc tgcgcgcgt 960
1183 gacgcaccgt gccggaaacg gtgcctatgg cgagaccgcc gttcgggtgg ggtggagaat 1020
1184 ggagaacaag gagcatcatt ggctcgcgtc ggtgagcagg agaaccgaact atttgcca 1080
1185 ttgccgtgac agatgggggg tgttactgc gtggagccgc gctgacaaat ga 1132
06 <210> SEQ ID NO: 32
07 <211> LENGTH: 373
08 <212> TYPE: PRT
09 <213> ORGANISM: Nicotiana tabacum
11 <400> SEQUENCE: 32
12 Met Ala Ile Glu His Asn Glu Gln Gln Leu Ser Gln Ser Phe Leu
13 1 5 10 15
15 Leu Asp Ala Leu Tyr Cys Glu Glu Glu Glu Glu Lys Trp Gly Asp Leu

```

*see item 9 on Ema Summary Sheet*

*P.3*

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/665,308A

DATE: 07/31/2001  
TIME: 14:45:58

Input Set : A:\BB1149USNA Corrected S q List.txt  
Output Set: N:\CRF3\07312001\I665308A.raw

```

1616          20          25          30
1618 Val Asp Asp Glu Thr Ile Ile Thr Pro Leu Ser Ser Glu Val Thr Thr
1619          35          40          45
1621 Thr Thr Thr Thr Thr Thr Lys Pro Asn Ser Leu Leu Pro Leu Leu Leu
1622          50          55          60
1624 Leu Glu Gln Asp Leu Phe Trp Glu Asp Glu Glu Leu Leu Ser Leu Phe
1625 65          70          75          80
1627 Ser Lys Glu Lys Glu Thr His Cys Trp Phe Asn Ser Phe Gln Asp Asp
1628          85          90          95
1630 Ser Leu Leu Cys Ser Ala Arg Val Asp Ser Val Glu Trp Ile Leu Lys
1631          100         105         110
1633 Val Asn Gly Tyr Tyr Gly Phe Ser Ala Leu Thr Ala Val Leu Ala Ile
1634          115         120         125
1636 Asn Tyr Phe Asp Arg Phe Leu Thr Ser Leu His Tyr Gln Lys Asp Lys
1637          130         135         140
1639 Pro Trp Met Ile Gln Leu Ala Ala Val Thr Cys Leu Ser Leu Ala Ala
1640 145         150         155         160
1642 Lys Val Glu Glu Thr Gln Val Pro Leu Leu Asp Phe Gln Val Glu
1643          165         170         175
1645 Asp Ala Lys Tyr Val Phe Glu Ala Lys Thr Ile Gln Arg Met Glu Leu
1646          180         185         190
1648 Leu Val Leu Ser Ser Leu Lys Trp Arg Met Asn Pro Val Thr Pro Leu
1649          195         200         205
1651 Ser Phe Leu Asp His Ile Ile Arg Arg Leu Gly Leu Arg Asn Asn Ile
1652          210         215         220
1654 His Trp Glu Phe Leu Arg Arg Cys Glu Asn Leu Leu Leu Ser Ile Met
1655 225         230         235         240
1657 Ala Asp Cys Arg Phe Val Arg Tyr Met Pro Ser Val Leu Ala Thr Ala
1658          245         250         255
1660 Ile Met Leu His Val Ile His Gln Val Glu Pro Cys Asn Ser Val Asp
1661          260         265         270
1663 Tyr Gln Asn Gln Leu Leu Gly Val Leu Lys Ile Asn Lys Glu Lys Val
1664          275         280         285
1666 Asn Asn Cys Phe Glu Leu Ile Ser Glu Val Cys Ser Lys Pro Ile Ser
1667          290         295         300
1669 His Lys Arg Lys Tyr Glu Asn Pro Ser His Ser Pro Ser Gly Val Ile
1670 305         310         315         320
1672 Asp Pro Ile Tyr Ser Ser Glu Ser Ser Asn Asp Ser Trp Asp Leu Glu
1673          325         330         335
1675 Ser Thr Ser Ser Tyr Phe Pro Val Phe Lys Lys Ser Arg Val Gln Glu
1676          340         345         350
1678 Gln Gln Met Lys Leu Ala Ser Ser Ile Ser Arg Val Phe Val Glu Ala
1679          355         360         365
1681 Val Gly Ser Pro His
1682          370
1685

```

Use of n and/or Xaa has been detected in the Sequence Listing.  
Review the Sequence Listing to insure a corresponding  
amino acid is represented in the <110> to <220> fields of  
each sequence using n or Xaa.



## VERIFICATION SUMMARY

DATE: 07/31/2001

PATENT APPLICATION: US/09/665,308A

TIME: 14:45:55

Input Set : A:\BB1149USNA Corrected Seq List.txt

Output Set: N:\CRF3\07312001\I665308A.raw

M:270 C: Current Application Number differs, Replaced Current Application No  
M:271 C: Current Filing Date differs, Replaced Current Filing Date  
M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3  
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3  
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3  
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3  
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3  
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3  
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4  
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4  
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4  
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M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
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M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
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M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8  
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M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9  
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15  
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15  
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16  
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/665,308A

DATE: 07/31/2001  
TIME: 14:45:59

Input Set : A:\BB1149USNA Corrected Seq List.txt  
Output Set: N:\CRF3\07312001\I665308A.raw

M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17  
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17  
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19  
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19  
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19  
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19  
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19  
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:20  
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
~~M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:20~~  
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:20  
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:789 SEQ:21  
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:22  
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:22  
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:22  
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23  
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
I:252 E: No. of Seq. differs, <211>LENGTH:Input:603 Found:1132 SEQ:23  
I:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25  
I:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
I:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25  
I:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
I:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25  
I:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
I:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26  
I:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
I:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26  
I:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
I:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26  
I:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
I:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:32